Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

1. (**Previously Presented**) A method for reducing false positives in the identification of at least one member of a pair or complex of interacting molecules from potentially interacting molecules, comprising:

(A) providing at least one set of host cells, each set containing at least one genetic element comprising a selectable marker, said selectable marker being different between different sets of host cells, said genetic element comprising a nucleic acid encoding one of said potentially interacting molecules, said host cells further carrying a readout system that is activated upon the presence of auto-activating molecules;

(B) transferring at least one set of said host cells or progeny of at least one set of said host cells to at least one selective medium, different for each set of host cells, which allows growth of said host cells in the presence of said genetic element comprising a selectable marker and which precludes growth of said host cells upon auto-activation of said readout system, thereby selecting against host cells expressing a molecule able to auto-activate the readout system;

(C) combining in said host cells at least two said genetic elements, wherein at least one set of said host cells with one of said at least two genetic elements undergoes the selecting step as specified in (B);

(D) allowing at least one interaction between said potentially interacting molecules, if any, to occur;

(E) selecting for said interaction by transferring said host cells or progeny of said host cells to a selective medium that allows identification of said host cells upon activation of the readout system;

(F) identifying host cells that contain interacting molecules that activate said readout system on said selective medium;

(G) identifying at least one member of said pair or complex of interacting molecules;

wherein said host cells are not yeast cells.

2. (**Previously Presented**) A method for reducing false positives in the identification of at least one member of a pair or complex of interacting molecules from potentially interacting molecules, comprising:

(A) providing at least one set of host cells, each set containing at least one genetic element comprising a selectable marker, said selectable marker being different between different sets of host cells, said genetic elements each comprising a nucleic acid encoding one of said potentially interacting molecules, said host cells further carrying a readout system that is activated upon the presence of auto-activating molecules;

(B) selecting against host cells expressing a molecule able to auto-activate the readout system by transferring at least one set of said host cells or progeny of at least one set of said host cells to at least one selective medium, different for each set of host cells, which allows growth of said host cells in the presence of said genetic element comprising a selectable marker and visual differentiation between those cells whose readout system has been activated from those host cells whose readout system has not been activated;

(C) combining in said host cells at least two different genetic elements, wherein at least one set of said host cells with one of said at least two genetic elements undergoes the selecting step as specified in (B);

(D) allowing at least one interaction between said potentially interacting molecules, if any, to occur;

(E) selecting for said interaction by transferring said host cells or progeny of said host cells to a selective medium that allows identification of said host cells upon activation of the readout system;

(F) identifying host cells that contain interacting molecules that activate said readout system on said selective medium;

(G) identifying at least one member of said pair or complex of interacting molecules.

3. **(Cancelled)**

4. **(Previously Presented)** The method of claim 1, wherein said pair or complex of interacting molecules is selected from RNA-RNA, RNA-DNA, RNA-protein, DNA-DNA, DNA-protein, protein-peptide, peptide-peptide or protein-protein interactions.

5. **(Previously Presented)** The method of claim 1, wherein said genetic element is a plasmid, artificial chromosome, virus or other extrachromosomal element.

6. **(Previously Presented)** The method of claim 1, wherein said interaction leads to the formation of a transcriptional activator that comprises a DNA-binding domain and a transactivating protein domain and is capable of activating a response moiety driving the activation of said readout system, wherein said DNA-binding domain and said transactivating protein domain are separately encoded by said at least two different genetic elements.

7. **(Original)** The method of claim 1, wherein said readout system comprises at least one counter-selectable gene.

8. **(Original)** The method of claim 7, wherein said counterselectable gene is one of the genes URA3, LYS2, sacB, CAN1, CYH2, rpsL, or lacY.

9. **(Original)** The method of claim 7, wherein the selective medium in step (B) comprises a counterselective compound.

10. **(Previously Presented)** The method of claim 9, wherein said counterselective compound is 5-fluoroorotic acid, canavanine, cycloheximide, sucrose, 2-nitrophenyl-β-D-thiogalactosidase (tONPG) or streptomycin.

11. **(Original)** The method of claim 2, wherein said readout system comprises or further comprises at least one detectable protein.

12. **(Previously Presented)** The method of claim 11, wherein said detectable protein is encoded from at least one of the genes lacZ, HIS3, URA3, LYS2, tetA, sacB, gfp (green fluorescent protein), yfp (yellow fluorescent protein), bfp (blue fluorescent protein), CAT (chloramphenicol acetyltransferase), luxAB, HPRT (hypoxanthine phosphoribosyltransferase), bla (β-lactamase), kan (kanamycin) or a surface marker.

13. **(Original)** The method of claim 1, wherein said host cells are bacterial cells, mammalian cells, insect cells or plant cells.

14. **(Original)** The method of claim 1, further comprising transforming, infecting or transfecting at least one set of host cells of said sets of host cells with said genetic element or genetic elements prior to step (D).

15. **(Original)** The method of claim 1, further comprising transforming, infecting or transfecting each set of host cells of said sets of host cells with said genetic elements prior to step (D).

16. **(Original)** The method of claim 1, further comprising transforming, infecting or transfecting one set of host cells of said sets of host cells with at least one genetic element prior to step (A), selecting against host cells in said one set of host cells expressing a molecule able to auto-activate said readout system as specified in step (B), and transforming, infecting or transfecting said set of host cells with at least one further genetic element in step (D).

17. **(Previously Presented)** The method of claim 1, wherein cell fusion, conjugation or interaction mating is used for the generation of said host cells with said genetic elements prior to step (D).

18. **(Original)** The method of claim 17, wherein said cell fusion, conjugation or interaction mating is affected or assisted by automation.

19. **(Previously Presented)** The method of claim 18, wherein said automation is effected by an automated process including picking, spotting, rearraying pipetting, micropipetting, or cell sorting.

20. **(Previously Presented)** The method of claim 19, wherein said process is effected by a picking robot, spotting robot, rearraying robot, pipetting system, micropipetting system or fluorescent assisted cell sorting (FACS) system.

21. **(Original)** The method of claim 1, wherein said selectable marker is an auxotrophic or antibiotic marker.

22. (**Original**) The method of claim 21, wherein said auxotrophic or antibiotic marker is LEU2, TRP1, URA3, ADE2, HIS3, LYS2, kan (kanamycin), bla (β-lactamase), Zeocin, neomycin, hygromycin, pyromycin or G418.

23. (**Original**) The method of claim 1, wherein host cells or progeny of host cells of step (D) are transferred to a storage compartment.

24. (**Original**) The method of claim 23, wherein the transfer to a storage compartment is effected or assisted by automation.

25. (**Previously Presented**) The method of claim 23, wherein the transfer to a storage compartment is effected by an automated process including arraying, replicating, picking, spotting, pipetting or micropipetting, or cell sorting.

26. (**Previously Presented**) The method of claim 25, wherein said process is effected by a picking robot, spotting robot, pipetting system, micropipetting system or fluorescent assisted cell sorting (FACS) system.

27. (**Original**) The method of claim 23, wherein said storage compartment comprises an anti-freeze agent.

28. (**Original**) The method of claim 23, wherein said storage compartment is at least one microtitre plate.

29. (**Original**) The method of claim 28, wherein said at least one microtitre plate comprises 96, 384, 846 or 1536 wells.

30. (**Original**) The method of claim 1, wherein the transfer of host cells or progeny of host cells in step (E) is effected or assisted by automation using a regular grid pattern.

31. (**Previously Presented**) The method of claim 30, wherein the transfer of host cells or progeny of host cells in step (E) is effected by an automated process including replicating, picking, spotting, pipetting or micropipetting, or cell sorting.

32. (**Previously Presented**) The method of claim 31, wherein said process is effected by a replicating robot, picking robot, spotting robot, pipetting system, micropipetting system or fluorescent assisted cell sorting (FACS) system.

33. (**Original**) The method of claim 30, wherein the transfer of host cells or progeny of host cells in step (E) is made by multiple transfers carrying additional host cells to the same position in said regular grid pattern.

34. (**Previously Presented**) The method of claim 1, wherein the transfer of host cells or progeny of host cells in step (E) is made to at least one carrier using a regular grid pattern.

35. (**Previously Presented**) The method of claim 34, wherein said at least one carrier is a microtitre plate and the regular grid pattern is at densities greater than 1 clone per square centimeter.

36. (**Previously Presented**) The method of claim 34, wherein said at least one carrier is a porous support and the regular grid pattern is at densities in the range of 1 to 10 clones per square centimeter.

37. (**Previously Presented**) The method of claim 34, wherein said at least one carrier is a non-porous support and the regular grid pattern is at densities in the range of 1 to 100 clones per square centimeter.

38. (**Previously Presented**) The method of claim 1 or claim 2, wherein the identification of host cells in step (F) for consideration of the activation state of said readout system is effected or assisted by an automated visual means.

39. (**Previously Presented**) The method of claim 1 or claim 2, wherein the identification of host cells in step (F) from consideration of the activation state of said readout system is effected or assisted by an automated process including digital image capture, digital storage, digital processing and/or digital analysis.

40. (**Original**) The method of claim 1, wherein the identification of said at least one member of said pair or complex of interacting molecules in step (G) is effected by nucleic acid hybridisation, oligonucleotide hybridisation, nucleic acid or protein sequencing, restriction digestion, spectrometry or antibody reactions.

41. (**Previously Presented**) The method of claim 1, wherein the identification of said at least one member of said pair or complex of interacting molecules in step (G) is effected using a regular grid pattern of said at least one member or of said nucleic acids encoding said at least one member.

42. **(Original)** The method of claim 41, wherein construction of regular grid patterns in step (G) is effected or assisted by automation.

43. **(Previously Presented)** The method of claim 42, wherein the automation is effected or assisted by an automated process including spotting, pipetting or micropipetting, or cell sorting.

44. **(Original)** The method of claim 43, wherein automation in step (G) is implemented by employing a spotting robot, spotting tool, pipetting system or micropipetting system.

45. **(Previously Presented)** The method of claim 41, wherein said identification is effected by an automated process including digital image capture, digital storage, digital processing and/or digital analysis.

46. **(Original)** The method of claim 1, wherein nucleic acid molecules, prior to said identification in step (G), are amplified by PCR or are amplified in a different host cell as a part of said genetic element or genetic elements.

47. **(Previously Presented)** The method of claim 1, further comprising:

(H) providing at least one of said genetic element in step (A), which additionally comprises or comprise a counter-selectable marker, wherein said counter-selectable markers are different for genetic elements associated with different sets of host cells;

(I) selecting for interaction by transferring host cells or progeny of host cells in step (E) to

(i) at least one selective medium that precludes growth of host cells in the presence of the counter-selectable marker associated with said genetic element specified in (H) and allows growth in the presence of a selectable marker associated with another of said at least two genetic elements in step (C); and

(ii) a further selective medium that allows identification of host cells upon activation of the readout system;

(J) identifying host cells in step (F) that contain interacting molecules that:

(iii) do not activate said readout system on said at least one selective medium specified in (i); and

(iv) activate said readout system on said selective medium specified in (ii).

48. (**Previously Presented**) The method of claim 47, wherein the genetic element that additionally comprises a counter-selectable marker further encodes an activation domain fusion protein.

49. (**Previously Presented**) The method of claim 1, further comprising:

(K) providing at least two of said genetic elements in step (A), which additionally comprise different counter-selectable markers;

(L) selecting for interaction by transferring host cells or progeny of host cells in step (E) to

(v) at least one selective medium that precludes growth of host cells in the presence of the first counterselectable marker of the counterselectable markers specified in (K) and allows growth in the presence of a first selectable marker;

(vi) at least one selective medium that precludes growth of host cells in the presence of the second counterselectable marker of the counterselectable markers specified in (K) and allows growth in the presence of a second selectable marker;

(vii) a further selective medium that allows identification of said host cells upon activation of the readout system; and

(M) identifying host cells that contain molecules that:

(viii) do not activate said readout system on said at least one selective medium specified in (v); and

(ix) do not activate said readout system on said at least one selective medium specified in (vi); and

(x) activate said readout system on said selective medium specified in (vii).

50. (**Previously Presented**) The method of claim 49, wherein said at least two genetic elements that additionally comprise a counter-selectable marker further encode a DNA binding domain fusion protein and an activation domain fusion protein, respectively.

51. (**Previously Presented**) The method of claim 47 or 49, wherein said counter-selectable marker or counter-selectable markers of step (H) or (K) are selected from the group of URA3, LYS2, sacB, CAN1, CYH2, rpsL or lacY.

52. (**Previously Presented**) The method of claim 47 or 49, wherein the transfer of host cells or progeny of host cells in step (I) or (L) is effected or assisted by automation.

53. (**Previously Presented**) The method of claim 52, wherein the said automation in step (I) or (L) is effected by an automated process including replicating, picking, spotting, pipetting or micropipetting, or cell sorting.

54. (**Original**) The method of claim 53, wherein said automation in step (I) or (L) is implemented by employing a replicating robot, picking robot, spotting robot, spotting tool, automated pipetting or micropipetting system, or fluorescent assisted cell sorting (FACS) system.

55. (**Original**) The method of claim 2, wherein said visual differentiation in step (B) is based on a difference between host cells in different activation states of the readout system which can be detected by visual means.

56. (**Previously Presented**) The method of claim 55, wherein said difference between host cells in different activation states that can be detected by visual means is brought about by activation of one of the genes lacZ, gfp (green fluorescent protein), yfp (yellow fluorescent protein), bfp (blue fluorescent protein), CAT (chloramphenicol acetyltransferase), luxAB, or of a surface marker.

57. (**Previously Presented**) The method of claim 55, wherein said visual means include digital image capture, digital storage, digital processing and/or digital analysis.

58. (**Previously Presented**) The method of claim 1, wherein said nucleic acid encoding one of said potentially interacting molecules is different for each host cell in a set of host cells or a majority of host cells in a set of host cells.

59. **(Previously Presented)** The method of claim 58, wherein said nucleic acid encoding one of said potentially interacting molecules is identical in not more than 10% of host cells in a set of host cells.

60-62. **(Canceled)**

63. **(Previously Presented)** A kit comprising:

(A) host cells, comprising a readout system which allows host cells to be counter-selected against auto-activation of said readout system; and

(B) at least one genetic element comprising a selectable marker, a counter-selectable marker and a nucleic acid encoding an activation domain or a DNA binding domain, which activation domain and DNA binding domain are together able to activate said readout system;

wherein said host cells are not yeast cells.

64. **(Previously Presented)** A kit according to claim 63, wherein said host cells are bacterial cells.

65-67. **(Canceled)**

68. **(Previously Presented)** The method of claim 17, wherein cell fusion, conjugation or interaction mating is used for the generation of said host cells with said genetic elements in step (C).

69. **(Previously Presented)** The method of claim 35, wherein said regular grid pattern is at a density greater than 4 clones per square centimeter.

70. **(Previously Presented)** The method of claim 69, wherein said regular grid pattern is at a density greater than 10 clones per square centimeter.

71. **(Previously Presented)** The method of claim 70, wherein said regular grid pattern is at a density greater than 18 clones per square centimeter.

72. **(Previously Presented)** The method of claim 36, wherein said regular grid pattern is at a density in the range of 10 to 50 clones per square centimeter.

73. **(Previously Presented)** The method of claim 72, wherein said regular grid pattern is at a density in the range of 50 to 100 clones per square centimeter.

74. **(Previously Presented)** The method of claim 73, wherein said regular grid pattern is at a density in the range of greater than 100 clones per square centimeter.

75. **(Original)** The method of claim 37, wherein said regular grid pattern is at a density in the range of 100 to 500 clones per square centimeter.

76. **(Previously Presented)** The method of claim 75, wherein said regular grid pattern is at a density in the range of 500 to 1000 clones per square centimeter.

77. **(Previously Presented)** The method of claim 76, wherein said regular grid pattern is at a density in the range of greater than 1000 clones per square centimeter.

78. **(Previously Presented)** The method of claim 46, wherein the amplification is carried out in a bacterial host cell.

79. **(Previously Presented)** The method of claim 78, wherein the bacterial host cell is *E. coli*.

80. **(Previously Presented)** The method of claim 59, wherein said nucleic acid encoding one of said potentially interacting molecules is identical in not more than 5% of host cells in a set of host cells.

81. **(Previously Presented)** The method of claim 80, wherein said nucleic acid encoding one of said potentially interacting molecules is identical in not more than 2% of host cells in a set of host cells.

82. **(Previously Presented)** The method of claim 81, wherein said nucleic acid encoding one of said potentially interacting molecules is identical in not more than 1% of host cells in a set of host cells.

83. **(Cancelled)**

84. **(Previously Presented)** A kit comprising:

(A) at least one genetic element, comprising a multiple cloning site connected to an entity which encodes a part of a readout system, which part of a readout system is capable to activate the readout system when fused to an auto-activating molecule, and further comprising a selectable marker; and

(B) instructions to

(i) clone nucleic acid encoding at least one potentially auto-activating molecule into said at least one genetic element of (A), and transform or transfect the resulting genetic element, or the resulting genetic elements, into at least one set of host cells, said host cells carrying a readout system which allows the visual differentiation of host cells in different activation states of the readout system, wherein different host cells comprise different nucleic acid encoding a potentially auto-activating molecule; and different sets of host cells comprise different selectable markers; and

(ii) differentiate host cells expressing an auto-activating molecule from host cells not expressing an auto-activating molecule, by transferring at least one set of host cells or progeny of at least one set of host cells to at least one medium, different for each set of host cells, which allows growth of said host cells in the presence of said selectable marker and allows visual differentiation between those cells whose readout system has been activated, from those host cells whose readout system has not been activated.

85. **(Previously Presented)** The kit of claim 84, further comprising at least one set of host cells, said host cells carrying a readout system which allows the visual differentiation of host cells in different activation states of the readout system.

86. **(Previously Presented)** The method of claim 1, wherein in step (C), each set of host cells with one of said at least two genetic elements undergoes the selecting step as specified in (B).

87. **(Previously Presented)** The method of claim 2, wherein in step (C), each set of host cells with one of said at least two genetic elements undergoes the selecting step as specified in (B).

88. **(Previously Presented)** The method of claim 6, wherein in step (C), said DNA-binding domain is encoded by one of said at least two genetic elements undergone the selecting step as specified in (B).